

REMARKS

The Examiner has maintained the restriction requirement. In accordance with the Examiner's maintenance of this requirement, Applicants herein cancel non-elected claims 44 and 60. Claims 8 and 51 have been cancelled herein and claims 10 and 15; 46; and 53, 55, 57, and 58 have been amended to properly depend from pending claims 16, 45, and 59, respectfully. No new matter has been added by virtue of the amendments as support lies in the original claims as filed as well as the specification. Claims 2-4, 6-7, 10-16 and 45-47, 49-50, and 53-59 remain pending and under consideration.

Applicants appreciate the Examiner's withdrawal of rejection of claims 10 and 53 under 35 USC 112, second paragraph.

Claims 2-16 and 45-59 were rejected under 35 USC 112, first paragraph as failing to comply with the written description requirement. The rejection is traversed.

The Examiner has maintained the rejection for written description and analogizes the present situation as akin to that of *University of Rochester v Searle & Co.*, (Fed. Cir., Feb. 13, 2004). In *Rochester*, however, no structural characteristics were set forth for any of the molecules which were encompassed within the *claimed subject matter*, rather the objection was grounded in the fact that the claimed subject matter was not supported by any structural definition, partial or otherwise, and based solely on a description of function. Applicants submit the present specification is certainly not in the same situation. Applicants respectfully point out the claimed subject matter at issue in the present application does in fact provide both structural and functional parameters from which to measure and assess polypeptides.

The Examiner objects to what structural features have been provided. Applicants submit the description of a polypeptide having at least 90% homology to either the entire sequence of SEQ ID NO:2 or at least 50 consecutive amino acids of SEQ ID NO:2 is clear to those of skill in the art. Those skilled in the art would readily recognize using only routine analysis polypeptides which fall within the genus of those polypeptides having such structural similarity. While more than one polypeptide falls within this range of structural homology, the determination to those of skill in the art of structural features which would fall within the scope is certainly clear and readily discernable.

Still further, Applicants have included limitations with a requirement of bioactivity of each of the claimed polypeptides. Applicants point out that independent claims 2, 16, 45, and 59 recite not only homology limitations relating to structural limitations of SEQ ID NO:2 variants, but also recite such sequence have "at least one bioactivity of an ACE2 polypeptide," thus reciting a combination of at least a partial structural features of a genus of polypeptides, as well as the biological activities of the polypeptides. The Examiner does not contradict that the level of skill in the art is high, and the disclosure

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of the application as filed provides sufficient description relating to the generation of variant sequences, nor that it is routine in the art to construct derivatives which are at least 90% identity to a given sequence (e.g., SEQ ID NO:2), or whether applicants have provided description in creating variants of SEQ ID NO:2 as well as polypeptides having at least 90% identity to the entire amino acid sequence set forth in SEQ ID NO:2 (see, e.g., specification last full paragraph page 43 through page 51). The Examiner merely contends a core sequence that each homologue must contain is required. Applicants submit this is not the standard, but one that would be required if the claimed molecules were described by structure alone. Applicants submit the correct standard is that if one skilled in the art would recognize the scope of what is claimed in view of the description; and with the presently claimed subject matter setting forth partial structure as well as bioactivity such standard has in fact been met.

Applicants respectfully request reconsideration and withdrawal of the rejection.

Claims 2-16 and 45-59 were rejected under 35 USC 112, first paragraph as failing to comply with the enablement requirement. The rejection is traversed.

The Examiner has maintained the rejection for failure to meet the requirements of the enablement standard, asserting that one would not know which residues to add/subtract/change to maintain the desired activity, and that testing all the peptides is undue. Applicants respectfully disagree. As outlined in Applicants' prior response, while there may be numerous possibilities of peptides which fall within the structural parameters set forth in the claimed subject matter, the generation of all possibilities as well as assessment of bioactivities of the peptides would be no more than routine in view of the knowledge in the art in combination with Applicants' teaching. Applicants have provided guidance regarding generation of each of the possible derivatives of SEQ ID NO:2 which are at least 90% identical to SEQ ID NO:2, and/or would be well understood to one of skill in the art in view of the provided description in combination with the knowledge and skill in the art. For example, Applicants have provided the amino acid sequence of SEQ ID NO:2. It is routine in the art to construct derivatives which are at least 90% identity to a given sequence (e.g., SEQ ID NO:2), and applicants have additionally provided description in creating variants of SEQ ID NO:2 as well as polypeptides having at least 90% identity to the entire amino acid sequence set forth in SEQ ID NO:2 (see, e.g., specification at page 29, first full paragraph through page 34, first full paragraph; and page 43, last full paragraph through page 51). Still further, Applicants' description sets forth the claimed bioactivities, as well as methods for assessing such activities (see, e.g., page 18, last paragraph through page 19; page 31, second full paragraph).

The Examiner's maintained rejection is still seemingly apparently based on there being numerous possibilities of various polypeptides comprising at least 90% identity to amino acid sequence of SEQ ID NO: 2 which could be generated, and testing whether these could each be assessed for biological activity, asserting the number of possibilities is exceeding the normal. Additionally, the Examiner states computer

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analysis alone is not sufficient for design. Applicants point out the combination of structure as well as activity distinguishes the present situation from that outlined by the examiner as solely computer modeling.

As discussed above, the number alone does not determine excessive, rather excessive or undue experimentation is determined in view of the state of the art. Applicants submit, the number of possibilities of testing alone is not sufficient to maintain the present enablement rejection, as the tools to carry out such generation and/or identification of peptides, testing of bioactivities and identification of polypeptides having at least 90% identity to amino acid sequence of SEQ ID NO:2 and having an ACE2 bioactivity are in fact readily available to those of skill in the art in view of Applicants' disclosure and the knowledge of those skilled in the art, and while such testing may take time and require testing of numerous possibilities, it remains to be routine testing nonetheless. Reconsideration and withdrawal of the rejection is thus respectfully requested.

This paper is being filed timely and it is believed no additional fees or extensions of time are required. In the event any additional fees or extensions of time are necessary, the undersigned hereby authorizes the requisite fees to be charged to Deposit Account No. 501668.

Entry of the remarks made herein is respectfully requested.

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Respectfully submitted,

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